



032796-019.ST25

SEQUENCE LISTING

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Little, Randall D.
Recker, Robert R.
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<120> REGULATING LIPID LEVELS VIA THE ZMAX1 OR HBM GENE

<130> 032796-019

<140> US 09/578,900

<141> 2000-05-26

<150> US 09/543,771

<151> 2000-04-05

<150> US 09/229,319

<151> 1999-01-13

<150> US 60/071,449

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<151> 1998-10-23

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<213> Homo sapiens

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Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
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Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
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ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
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Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
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cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc gcc ctg gtc tct 397
Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser

95	100	105	445
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Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr			
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gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc			493
Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser			
130	135	140	
cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc			541
Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala			
145	150	155	
ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg ggt gag acg			589
Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr			
160	165	170	
ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att			637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile			
175	180	185	
gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag			685
Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu			
190	195	200	
gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt			733
Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg			
210	215	220	
gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg			781
Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu			
225	230	235	
acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca			829
Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr			
240	245	250	
gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg			877
Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly			
255	260	265	
aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag			925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln			
270	275	280	
gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag			973
Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu			
290	295	300	
gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct			1021
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro			
305	310	315	
ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc			1069
Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly			
320	325	330	
agg acg tgt aag gca gga gcc gag gag gtg ctg ctg gcc cgg cgg			1117
Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg			
335	340	345	
acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc			1165
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile			
350	355	360	
gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac			1213
Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp			
370	375	380	
ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc			1261
Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile			
385	390	395	
cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc			1309
Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr			

400	405	410	
gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac			1357
Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn			
415	420	425	
ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc			1405
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu			
430	435	440	445
aac ggc acc tcc cgc aag atc ctg gtg tgc gag gac ctg gac gag ccc			1453
Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro			
450	455	460	
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac			1501
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp			
465	470	475	
tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag			1549
Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu			
480	485	490	
cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc			1597
Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala			
495	500	505	
ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac			1645
Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp			
510	515	520	525
aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg			1693
Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu			
530	535	540	
gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc			1741
Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe			
545	550	555	
atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag			1789
Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys			
560	565	570	
gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg			1837
Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met			
575	580	585	
ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt			1885
Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys			
590	595	600	605
gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac			1933
Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His			
610	615	620	
gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg			1981
Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met			
625	630	635	
aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc			2029
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala			
640	645	650	
gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc			2077
Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile			
655	660	665	
ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc			2125
Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser			
670	675	680	685
aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc			2173
Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg			
690	695	700	
gcc ttc atg aac ggg agc tgc gtg gag cac gtg gtg gag ttt ggc ctt			2221
Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu			

705	710	715	2269
gac tac ccc gag ggc atg gcc gtt	gac tgg atg ggc aag aac ctc tac		
Asp Tyr Pro Glu Gly Met Ala Val	Asp Trp Met Gly Lys Asn Leu Tyr		
720	725	730	2317
tgg gcc gac act ggg acc aac aga atc	gaa gtg gcg cgg ctg gac ggg		
Trp Ala Asp Thr Gly Thr Asn Arg	Ile Glu Val Ala Arg Leu Asp Gly		
735	740	745	2365
cag ttc cgg caa gtc ctc gtg tgg agg	gac ttg gac aac ccg agg tgc		
Gln Phe Arg Gln Val Leu Val Trp	Arg Asp Leu Asp Asn Pro Arg Ser		
750	755	760	2413
ctg gcc ctg gat ccc acc aag ggc tac	atc tac tgg acc gag tgg ggc		
Leu Ala Leu Asp Pro Thr Lys Gly Tyr	Ile Tyr Trp Thr Glu Trp Gly		
770	775	780	2461
ggc aag ccg agg atc gtg cgg gcc ttc	atg gac ggg acc aac tgc atg		
Gly Lys Pro Arg Ile Val Arg Ala Phe	Met Asp Gly Thr Asn Cys Met		
785	790	795	2509
acg ctg gtg gac aag gtg ggc cgg gcc	aac gac ctc acc att gac tac		
Thr Leu Val Asp Lys Val Gly Arg Ala	Asn Asp Leu Thr Ile Asp Tyr		
800	805	810	2557
gct gac cag cgc ctc tac tgg acc gac	ctg gac acc aac atg atc gag		
Ala Asp Gln Arg Leu Tyr Trp Thr	Asp Leu Asp Thr Asn Met Ile Glu		
815	820	825	2605
tcg tcc aac atg ctg ggt cag gag cgg	gtc gtg att gcc gac gat ctc		
Ser Ser Asn Met Leu Gly Gln Glu Arg	Val Val Ile Ala Asp Asp Leu		
830	835	840	2653
ccg cac ccg ttc ggt ctg acg cag tac	agc gat tat atc tac tgg aca		
Pro His Pro Phe Gly Leu Thr Gln Tyr	Ser Asp Tyr Ile Tyr Trp Thr		
850	855	860	2701
gac tgg aat ctg cac agc att gag cgg	gcc gac aag act agc ggc cgg		
Asp Trp Asn Leu His Ser Ile Glu Arg	Ala Asp Lys Thr Ser Gly Arg		
865	870	875	2749
aac cgc acc ctc atc cag ggc cac ctg	gac ttc gtg atg gac atc ctg		
Asn Arg Thr Leu Ile Gln Gly His Leu	Asp Phe Val Met Asp Ile Leu		
880	885	890	2797
gtg ttc cac tcc tcc cgc cag gat ggc	ctc aat gac tgt atg cac aac		
Val Phe His Ser Ser Arg Gln Asp Gly	Leu Asn Asp Cys Met His Asn		
895	900	905	2845
aac ggg cag tgt ggg cag ctg tgc ctt	gcc atc ccc ggc ggc cac cgc		
Asn Gly Gln Cys Gly Gln Leu Cys Leu	Ala Ile Pro Gly Gly His Arg		
910	915	920	2893
tgc ggc tgc gcc tca cac tac acc ctg	gac ccc agc agc cgc aac tgc		
Cys Gly Cys Ala Ser His Tyr Thr Leu	Asp Pro Ser Ser Arg Asn Cys		
930	935	940	2941
agc ccg ccc acc acc ttc ttg ctg ttc	agc cag aaa tct gcc atc agt		
Ser Pro Pro Thr Thr Phe Leu Leu Phe	Ser Ser Gln Lys Ser Ala Ile Ser		
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cgg atg atc ccg gac gac cag cac agc	ccg gat ctc atc ctg ccc ctg		
Arg Met Ile Pro Asp Asp Gln His Ser	Pro Asp Leu Ile Leu Pro Leu		
960	965	970	3037
cat gga ctg agg aac gtc aaa gcc atc	gac tat gac cca ctg gac aag		
His Gly Leu Arg Asn Val Lys Ala Ile	Asp Tyr Asp Pro Leu Asp Lys		
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ttc atc tac tgg gtg gat ggg cgc cag	aac atc aag cga gcc aag gac		
Phe Ile Tyr Trp Val Asp Gly Arg Gln	Asn Ile Lys Arg Ala Lys Asp		
990	995	1000	3133
gac ggg acc cag ccc ttt gtt ttg acc	tct ctg agc caa ggc caa aac		
Asp Gly Thr Gln Pro Phe Val Leu Thr	Ser Leu Ser Gln Gly Gln Asn		

cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca	1010	1015	1020	3181
Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr				
ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg	1025	1030	1035	3229
Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu				
agc ggg gaa gcc atg ggg gtg gtg ctg cgt ggg gac cgc gac aag ccc	1040	1045	1050	3277
Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro				
agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac	1055	1060	1065	3325
Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn				
atg cag gac cgg gca gcc aag atc gaa cgc gca gcc ctg gac ggc acc	1070	1075	1080	3373
Met Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr				
gag cgc gag gtc ctc ttc acc acc ggc ctc atc cgc cct gtg gcc ctg	1090	1095	1100	3421
Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu				
gtg gtg gac aac aca ctg ggc aag ctg ttc tgg gtg gac gcg gac ctg	1105	1110	1115	3469
Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu				
aag cgc att gag agc tgt gac ctg tca ggg gcc aac cgc ctg acc ctg	1120	1125	1130	3517
Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu				
gag gac gcc aac atc gtg cag cct ctg ggc ctg acc atc ctt ggc aag	1135	1140	1145	3565
Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys				
cat ctc tac tgg atc gac cgc cag cag cag atg atc gag cgt gtg gag	1150	1155	1160	3613
His Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu				
aag acc acc ggg gac aag cgg act cgc atc cag ggc cgt gtc gcc cac	1170	1175	1180	3661
Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His				
ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca	1185	1190	1195	3709
Leu Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser				
gcc cac cca tgt gcc cgt gac aat ggt ggc tgc tcc cac atc tgt att	1200	1205	1210	3757
Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile				
gcc aag ggt gat ggg aca cca cgg tgc tca tgc cca gtc cac ctc gtg	1215	1220	1225	3805
Ala Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val				
ctc ctg cag aac ctg ctg acc tgt gga gag ccg ccc acc tgc tcc ccg	1230	1235	1240	3853
Leu Leu Gln Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro				
gac cag ttt gca tgt gcc aca ggg gag atc gac tgt atc ccc ggg gcc	1250	1255	1260	3901
Asp Gln Phe Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala				
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Trp Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu				
ggc tgc ccc gtg tgc tcc gcc gcc cag ttc ccc tgc gcg cgg ggt cag	1280	1285	1290	3997
Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln				
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Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp				

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Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe				
1330	1335	1340		
cgg tgt gcg agc ggc cag tgt gtc ctc atc aaa cag cag tgc gac tcc				4141
Arg Cys Ala Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser				
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Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr				
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Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro				
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gtc att ggc atc atc ctc tct ctc ttc gtc atg ggt ggt gtc tat ttt				4285
Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe				
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Val Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro				
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Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe				
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Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys				
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Gly Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly				
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Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser				
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Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro				
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Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr				
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tct tca aac att ccg gcc act gcg aga ccg tac agg ccc tac atc att				4669
Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile				
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cga gga atg gcg ccc ccg acg acg ccc tgc agc acc gac gtg tgt gac				4717
Arg Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp				
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agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat				4765
Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp				
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ttg aac tcg gac tca gac ccc tat cca ccc cca ccc acg ccc cac agc				4813
Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser				
1570	1575	1580		
cag tac ctg tcg gcg gag gac agc tgc ccg ccc tcg ccc gcc acc gag				4861
Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu				
1585	1590	1595		
agg agc tac ttc cat ctc ttc ccg ccc cct ccg tcc ccc tgc acg gac				4909
Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp				
1600	1605	1610		
tca tcc tgacctcggc cggggccactc tggcttctct gtgcccctgt aaatagtttt				4965
Ser Ser				

1615
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 Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
 1 5 10
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 Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
 15 20 25
 gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc ccg gac gta cgg ctg 205
 Ala Ala Ser Pro Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
 30 35 40 45
 gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc 253
 Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
 50 55 60
 ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
 Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
 65 70 75
 tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac 349
 Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
 80 85 90
 cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct 397
 Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
 95 100 105
 ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg 445
 Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr
 110 115 120 125
 gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc 493
 Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser
 130 135 140
 cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc 541
 Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala
 145 150 155
 ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg gtt gag acg 589
 Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr
 160 165 170
 ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att 637
 Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile
 175 180 185
 gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag 685
 Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu
 190 195 200 205
 gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt 733
 Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg
 210 215 220
 gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg 781
 Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu
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Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln	
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Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile	
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Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr	
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Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn	
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Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro	
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 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp 60
 50 55
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 65 70 75
 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly 95
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 100 105

Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
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 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
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 Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
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<223> Identity of nucleotide sequences at the above locations are unknown.

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agcgactgg ggggaagagg aaggagatcc tgagtgcct atactaccc atggacatcc 180
agggtgctgag ccaggagcgg cagccttttt gtgagtgcg g 221

<210> 44
<211> 156
<212> DNA
<213> Homo sapiens

<400> 44
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156

<210> 45
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 45
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 cacggaccgc atcgagggtga cgcgcctcaa cggcacctcc cgcaagatcc tgggtgtcgga 360
 ggacctggac gagccccgag ccatcgact gcaccccggt atggggtaag acgggc 416

<210> 46
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 46
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 ctggccctgg acctgcagga ggggaagctc tactggggag acgccaagac agacaagatc 180
 gaggtgaggg tcctgtgg 198

<210> 47
 <211> 244
 <212> DNA
 <213> Homo sapiens

<400> 47
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 gccgcagcat cgagcgggtg cacaaggtca aggccagcgg ggacgtcatc attgaccagc 180
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 ggtc 244

<210> 48
 <211> 313
 <212> DNA
 <213> Homo sapiens

<400> 48
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 aggtagcgtg ggc 313

<210> 49
 <211> 255
 <212> DNA
 <213> Homo sapiens

<400> 49
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 aagtgtttgc ctgtc 255

<210> 50
 <211> 210
 <212> DNA
 <213> Homo sapiens

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<210> 51
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 51
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 ggcagtgtgg gcagctgtgc cttgccatcc ccggcggcca ccgctgcggc tgcgcctcac 300
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<210> 52
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 52
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<210> 53
 <211> 235
 <212> DNA
 <213> Homo sapiens

<400> 53
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 <211> 218
 <212> DNA
 <213> Homo sapiens

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 gtggccctgg tgggtggaaa cacactgggc aagctgttct ggggtggacgc ggacctgaag 180
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 <212> DNA
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<210> 56
 <211> 157
 <212> DNA
 <213> Homo sapiens

<400> 56
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<210> 57
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 <212> DNA
 <213> Homo sapiens

<400> 57
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<210> 58
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 <212> DNA
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<400> 58
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 tggtagacca gctt 134

<210> 59
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 <212> DNA
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<400> 59
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 <211> 130
 <212> DNA
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<210> 62
 <211> 496
 <212> DNA
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<400> 62	
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ttaattttgt	aaaaca
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<210> 63
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 <212> DNA
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<220>
 <223> Artificial sequence is a primer.

<400> 63	
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<210> 64
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<220>

<223> Artificial sequence is a primer.

<400> 64
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<210> 65
<211> 24
<212> DNA
<213> Homo sapiens

<400> 65
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<210> 66
<211> 25
<212> DNA
<213> Homo sapiens

<400> 66
ggctcacgga gctcatcatg gactt 25

<210> 67
<211> 502
<212> DNA
<213> Homo sapiens

<400> 67
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<210> 68
<211> 21
<212> DNA
<213> Mouse

<400> 68
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<210> 69
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<212> DNA
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<400> 69
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<210> 70
<211> 501
<212> DNA
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<400> 70

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attgattatg ccgaccagcg a                                     501

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<210> 71

<211> 25

<212> RNA

<213> Mouse

<400> 71

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<210> 72

<211> 25

<212> RNA

<213> Mouse

<400> 72

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<210> 73

<211> 25

<212> RNA

<213> Mouse

<400> 73

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